In the Claims

A marked up copy of the claims as amended is shown below. Please cancel claims 10, 22 and 24 without prejudice or disclaimer. Please add new claims 31-46.

1. (currently amended) A method of determining at least one haplotype encompassing ~~of~~ a genetic coding locus comprising:

   (a) amplifying genomic DNA, wherein the amplified genomic DNA comprises a non-coding region sequence that is in genetic linkage with the genetic coding locus;

   (b) detecting one or more sequence variations in the non-coding region; and

   (c) using the one or more non-coding region sequence variations to determine ~~determining~~ at least one haplotype encompassing ~~of~~ the genetic coding locus.

2. (original) The method of claim 1, wherein a single haplotype is determined.

3. (original) The method of claim 1, wherein two or more haplotypes are determined.

4. (original) The method of claim 1, wherein the genetic locus is an HLA locus.

5. (original) The method of claim 1, wherein the at least one haplotype is associated with a genetic disease.

6. (original) The method of claim 5, wherein the disease is cystic fibrosis.

7. (original) The method of claim 5, wherein the disease is phenylketonuria, muscular dystrophy or beta-thalassemia.

8. (currently amended) The method of claim 1, further comprising ~~forensic testing~~ (i) detecting one or more sequence variations in the coding region of the locus; and (ii) using the one or more coding region sequence variations to determine at least one haplotype encompassing the genetic coding locus.

9. (currently amended) The method of claim 1 ~~8~~, further comprising:

(a) analyzing DNA from a crime scene sample;

(b) analyzing DNA from a sample of a suspected perpetrator of the crime; and

(c) comparing the haplotypes present in the crime scene sample and the suspected perpetrator sample.

10. (canceled)

11. (currently amended) The method of claim 1 ~~10~~, further comprising:

(a) analyzing DNA from an off-spring;

(b) analyzing DNA from at least one suspected parent; and

(c) comparing the haplotypes present in the offspring's DNA and in the suspected parent's DNA.

12. (original) The method of claim 1, wherein the amplified genomic DNA further comprises at least part of at least one exon.

13. (currently amended) A method for determining ~~determination of~~ at least one haplotype encompassing ~~of~~ a multi-allelic genetic coding locus comprising:

(a) amplifying genomic DNA with a primer pair that spans a non-coding region sequence, said primer pair defining a DNA sequence which is in genetic linkage with said genetic coding locus and contains a sufficient number of non-coding region sequence nucleotides to produce an amplified DNA sequence characteristic of said at least one haplotype;

(b) analyzing the amplified DNA sequence to detect one or more sequence variations in the non-coding region; and

(c) using the one or more non-coding region sequence variations to determine ~~determining~~ at least one haplotype encompassing ~~of~~ the multiallelic genetic coding locus.

14. (original) The method of claim 13, wherein a single haplotype is determined.

15. (original) The method of claim 13, wherein two or more haplotypes are determined.

16. (original) The method of claim 13, wherein the genetic locus is an HLA locus.

17. (original) The method of claim 13, wherein the at least one haplotype is associated with a genetic disease.

18. (original) The method of claim 17, wherein the genetic disease is associated with variations in a regulatory or other untranslated region of the genetic locus.

19. (currently amended) A method for determining ~~determination of~~ at least one haplotype encompassing ~~of~~ an HLA coding locus comprising:

(a) amplifying genomic DNA with a primer pair that spans a non-coding region sequence, said primer pair defining a DNA sequence which is in genetic linkage with said HLA coding locus;

(b) analyzing the amplified DNA sequence to detect one or more sequence variations in the non-coding region; and

(c) using the one or more non-coding region sequence variations to determine ~~determining~~ at least one haplotype encompassing ~~of~~ the HLA coding locus.

20. (original) The method of claim 19, wherein a single haplotype is determined.

21. (original) The method of claim 19, wherein two or more haplotypes are determined.

22. (canceled)

23. (currently amended) The method of claim 19~~22~~, further comprising:

(a) analyzing DNA from a crime scene sample;

(b) analyzing DNA from a sample of a suspected perpetrator of the crime; and

(c) comparing the haplotypes present in the crime scene sample and the suspected perpetrator sample.

24. (canceled)

25. (currently amended) The method of claim 19~~24~~, further comprising:

(i) analyzing DNA from an off-spring;

(ii) analyzing DNA from at least one suspected parent; and

(iii) comparing the haplotypes present in the offspring's DNA and in the suspected parent's DNA.

26. (previously added) The method of claim 1, wherein the haplotype is determined by detecting polymorphisms in coding and non-coding regions.

27. (previously added) The method of claim 1, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

28. (previously added) The method of claim 13, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

29. (previously added) The method of claim 19, wherein the haplotype is determined by detecting polymorphisms in coding and non-coding regions.

30. (previously added) The method of claim 19, wherein the non-coding region comprises an intervening sequence, a 5' untranslated sequence (5'-UTR), a 3'-UTR, a regulatory sequence or an intergenic sequence.

31. (new) A method for genetic analysis, comprising:

a) amplifying a non-coding region of genomic DNA with a primer pair to produce an amplified DNA sequence, wherein said non-coding region is in genetic linkage with one or more coding region alleles that confer a trait;

b) analyzing the amplified DNA sequence to detect genetic variation in the non-coding region; and

c) correlating the genetic variation in the non-coding region with the trait conferred by the one or more coding region alleles.

32. (new) The method of claim 31, wherein the trait is a genetic disease.

33. (new) The method of claim 31, wherein the trait is susceptibility to a disease.

34. (new) The method of claim 32, wherein the disease is monogenic.

35. (new) The method of claim 32, wherein the disease is multigenic.

36. (new) The method of claim 31, wherein the analyzing comprises hybridizing the amplified DNA sequence to an oligonucleotide.

37. (new) The method of claim 31, wherein the amplified DNA sequence is labeled.

38. (new) The method of claim 36, wherein the oligonucleotide is a sequence-specific oligonucleotide.

39. (new) The method of claim 36, wherein the amplified DNA sequence is hybridized with a plurality of oligonucleotides.

40. (new) The method of claim 31, wherein the genetic variation comprises a plurality of polymorphisms.

41. (new) The method of claim 40, wherein the plurality of polymorphisms comprise single base polymorphisms.

42. (new) The method of claim 31, wherein the non-coding region is remote from the coding region.

43. (new) The method of claim 42, wherein the method is performed on a plurality of non-coding regions from a selected chromosome region in different individuals.

44. (new) The method of claim 43, wherein (a) and (b) of the method are repeated for a plurality of non-coding regions from a second selected chromosome region from the different individuals.

45. (new) The method of claim 31, wherein the non-coding region is an intron sequence.

46. (new) The method of claim 31, wherein the non-coding region is a regulatory region.